

ID NINE, CAMEL STANDARD: PFT: 572 AA.
 AC Q134.CHEK
 DT 30-MAY-2000 (rel. 39, Created)
 DT 30-MAY-2000 (rel. 39, Last sequence update)
 DT 30-MAY-2001 (rel. 40, Last annotation update)
 DE NUCLEAR HORMONE RECEPTOR FAMILY MEMBER NHR-25
 GN NHR-25 OR FICL1.6 genes
 GN Eukaryota; Metazoa; Neomata; Chromalveola; Rhaditoidae;
 OC Rhaditoidae; Pelodielinae; Ctenohaditids.
 OC [1]-taxid=6239;
 RN SEQUENCE FROM N.A.
 RC STRAIN=SRISTOL NZ;
 CC - FUNCTION: ORPHAN NUCLEAR RECEPTOR.
 CC - FUNCTION: ORPHAN NUCLEAR RECEPTOR.
 CC - SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
 CC - THIS RECEPTOR IS A MEMBER OF THE NUCLEAR HORMONE RECEPTORS FAMILY.
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 CC or send an email to license@isb-sib.ch).
 CC EMBL: Z43270; CAA81028.1; ..
 DR HSP: P13793; ZML: 0003191.
 DR InterPro: IPR000139.
 DR InterPro: IPR000535; Hormone_rec_lig.
 DR InterPro: IPR001628; zf-C4.
 DR Pfam: PF00105; zf-C4_1; acc: 1.
 DR PRINTS: PR00447; STR01DFINGER.
 DR SMART: SMO0399; ZOP_C4_1.
 DR SMART: SMO0399; ZOP_C4_1.
 DR PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.
 DR Receptor; Transcription regulation; DNA-binding; Nuclear protein;
 KW DNA BINDING. 18 83 NUCLEAR RECEPTOR-TYPE.
 FT DNA BINDING 18 38 C4 TYPE.
 FT ZN BINDING 18 38 C4 TYPE.
 SQ SEQUENCE 572 AA: 64772 MW: 13052AEE33092D7A CRC64:
 Query Match 52.9%; Score 27; DR 1; Length 572;
 Best Local Similarity 23.3%; Pred. No. 32;
 Matches 4; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
 QY 2 CXXXXXXXXXXXXC 18
 DB 54 CAGACAGACAGACAGAC 70

RX MEDLINE-94103212; PubMed-7506255;
 AC The somatic cell-specific low density lipoprotein receptor-related
 DT protein of the chicken. Close kinship to mammalian low density
 DT lipoprotein receptor family members.*
 RL J Biol Chem. 269:213-219(1994).
 CC - FUNCTION: INVOLVED IN THE PLASMA CLEARANCE OF CHYLOMICRON REMNANTS
 CC AND IN THE CLEARANCE OF LOW DENSITY LIPOPROTEIN REMNANTS.
 CC METABOLISM OF COMPLEXES; BENES VITELLOGENIN, CALCIUM AND ALPHA 2-
 CC ENDOGENOUS INHIBITORS; BENES VITELLOGENIN, CALCIUM AND ALPHA 2-
 CC MICROGLOBULIN LOCATION: TYPE 1 MEMBRANE PROTEIN.
 CC - ALTERNATIVE PRODUCTS: IN CLONE N16, AN ASP IS REPLACED BY
 CC SER-GLY-ARG-GLN-ASP DUE TO ALTERNATIVE SPLICING OF EXONS.
 CC - PKA: CLEAVED INTO A 85 KDA MEMBRANE-SPANNING SUBUNIT (LBP-85) AND
 CC A 55 KDA LARGE EXTRACELLULAR DOMAIN (LBP-55) THAT REMAINS NON-
 CC - SIMILARITY: CONTAINS 32 BGF-LIKE DOMAINS.
 CC - SIMILARITY: CONTAINS 32 BGF-LIKE DOMAINS.
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 CC tion between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC EMBL: X74904; CAA52870.1; ..
 DR InterPro: IPR00152; Asx_hydroxyl.
 DR InterPro: IPR000561; BGF-Like.
 DR InterPro: IPR001818; BGF_CA.
 DR PRINTS: PR00198; BGF-Like.
 DR InterPro: IPR002172; LDL_recept_A.
 DR InterPro: IPR000033; LDL_recept_rep.
 DR Pfam: PF00059; LDL_recept_d; 31.
 DR Pfam: PF00059; LDL_recept_d; 31.
 DR PRINTS: PR00198; BGF-Like.
 DR PRINTS: PR00261; LDLRECEPTOR.
 DR SMART: SMO0179; BGF_CA; 3.
 DR SMART: SMO0182; BGF_Like; 18.
 DR SMART: SMO0135; Lr; 34.
 DR PROSITE: PS00010; ASX_HYDROXYL; 3.
 DR PROSITE: PS01187; BGF_CA; 2.
 DR PROSITE: PS01187; BGF_CA; 2.
 DR PROSITE: PS01186; BGF_2; 7.
 DR PROSITE: PS00068; LDLA; 31.
 DR Receptor; Transmembrane; Repeat; Endocytosis; Glycoprotein;
 KW Calcium-binding; BGF-Like domain; Coated pits;
 KW Altrative aplication; 21
 FT SIGNAL 22 4543 POTENTIAL.
 FT CHAIN 22 4543 LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED
 FT DOMAIN 22 4419 EXTRACELLULAR (POTENTIAL).
 FT TRANSFAM 4420 4443 POTENTIAL (POTENTIAL).
 FT TRANSFAM 4443 4468 POTENTIAL (POTENTIAL).
 FT DOMAIN 27 68 LDL-RECEPTOR CLASS A 1.
 FT DOMAIN 72 112 LDL-RECEPTOR CLASS A 2.
 FT DOMAIN 152 191 BGF-LIKE 1.
 FT DOMAIN 476 522 BGF-LIKE 3.
 FT DOMAIN 801 841 BGF-LIKE 4.
 FT DOMAIN 801 841 BGF-LIKE 4.
 FT DOMAIN 891 931 LDL-RECEPTOR CLASS A 3.
 FT DOMAIN 932 971 LDL-RECEPTOR CLASS A 4.
 FT DOMAIN 932 971 LDL-RECEPTOR CLASS A 5.
 FT DOMAIN 1011 1051 LDL-RECEPTOR CLASS A 6.
 FT DOMAIN 1011 1051 LDL-RECEPTOR CLASS A 7.
 FT DOMAIN 1058 1097 LDL-RECEPTOR CLASS A 8.

OY 2 CXXXXXXCXXXXC 18
 DB 252 CVDNECDASNCQACC 286
 RESULT 15
 ID FRIG BAT STANDARD: PPT: 493 AA.
 AC 03568: 2001 (Rel. 40, Created)
 DT 20-AUG-2001 (Rel. 40, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE EGF-CONTAINING FIBRIN-LIKE EXTRACELLULAR MATRIX PROTEIN 1 PRECURSOR
 GN EFEMP1 (OR FEK1)
 OS *Neftus norvegicus* (rat).
 OC *Neftus norvegicus*: Castella, Verhegden, Kuylenstierna,
 OC Mammalia: Eutheria: Rodentia, Sciurognathi: Muridae, Murinae: Murus.
 OX NCBI_TaxId=10116;
 RN 11
 RN SUBJECT FROM H.A.
 RC TISSUE=Lung;
 RX MEDLINE=97415782; PubMed=9268694;
 RA Sakiyama S, Iwano K., Nakamura T., Ichinoya S., Nakagawa A.,
 RA "Interaction of DA1, a DAN-binding protein, with the epidermal growth
 factor-like protein, S(1-5)."; 237-245-250(1997).
 RT 1- SUBCELLULAR LOCATION: SECRETED.
 CC -1- SIMILARITY: CONTAINS 6 EGF-LIKE DOMAINS.
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 CC
 DB 069730: BAA2265.1;
 DR EGF-CONTAINING FIBRIN-LIKE EXTRACELLULAR
 DR EGF-CONTAINING FIBRIN-LIKE EXTRACELLULAR
 DR INTERPRO: IPR001881, EGF-like.
 DR SMART: SM00179, EGF CA; 4.
 DR SMART: SM00001, EGF-like; 2.
 DR PROSITE: PS01166, EGF-CA; 4.
 DR PROSITE: PS01166, EGF-CA; 4.
 DR PROSITE: PS01167, EGF-CA; 6.
 DR PROSITE: PS01167, EGF-CA; 6.
 DR EGF-CONTAINING FIBRIN-LIKE EXTRACELLULAR
 DR EGF-CONTAINING FIBRIN-LIKE EXTRACELLULAR
 DR SIGNAL 1 17
 FT CHAIN 18 493 EGF-CONTAINING FIBRIN-LIKE EXTRACELLULAR
 FT DOMAIN 26 71 EGF-LIKE 1, DIVERGENT.
 FT DOMAIN 173 213 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 214 253 EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 254 294 EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 295 335 EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 336 376 EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 377 417 EGF-LIKE 7, CALCIUM-BINDING (POTENTIAL).
 FT DISULFID 184 190 BY SIMILARITY.
 FT DISULFID 201 212 BY SIMILARITY.
 FT DISULFID 218 228 BY SIMILARITY.
 FT DISULFID 239 252 BY SIMILARITY.
 FT DISULFID 258 268 BY SIMILARITY.
 FT DISULFID 269 279 BY SIMILARITY.
 FT DISULFID 298 309 BY SIMILARITY.
 FT DISULFID 305 318 BY SIMILARITY.
 FT DISULFID 320 332 BY SIMILARITY.

FT DISULFID 338 350 BY SIMILARITY.
 FT DISULFID 344 359 BY SIMILARITY.
 FT DISULFID 355 377 BY SIMILARITY.
 SQ SEQUENCE 493 AA: 54596 MW: 23047.076 DACTUCAS CRG04:
 Query Match 51.0%; Score 36; PW 1; Length 493;
 Best Local Similarity 23.5%; Prod. No. 50;
 Matches 4; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
 OY 2 CXXXXXXCXXXXC 18
 DB 252 CVDNECDASNCQACC 286

Search completed: February 13, 2002, 10:11:04
 Job time: 112 sec
